

re-run



IFWP

RAW SEQUENCE LISTING

DATE: 07/20/2006

PATENT APPLICATION: US/10/533,037

TIME: 19:15:29

Input Set : N:\Crf4\Refhold\10_folder\J533037.raw

Output Set: N:\CRF4\07202006\J533037.raw

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1 <110> APPLICANT: Chang, Chawnshang
2     Yi-Fen Lee
3     Wen-Jye Lin
4 <120> TITLE OF INVENTION: Hydroxyflutamide Induced Pathways
5     Related to Androgen Receptor Negative Prostate Cancer Cells
6 <130> FILE REFERENCE: 21108.0017U2
7 <140> CURRENT APPLICATION NUMBER: US/10/533,037
8 <141> CURRENT FILING DATE: 2005-04-28
9 <150> PRIOR APPLICATION NUMBER: PCT/US03/34636
10 <151> PRIOR FILING DATE: 2003-10-31
11 <150> PRIOR APPLICATION NUMBER: 60/423,340
12 <151> PRIOR FILING DATE: 2002-10-31
13 <160> NUMBER OF SEQ ID NOS: 28
14 <170> SOFTWARE: FastSEQ for Windows Version 4.0
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17 <211> LENGTH: 1587
18 <212> TYPE: DNA
19 <213> ORGANISM: Artificial Sequence
20 <220> FEATURE:
21 <223> OTHER INFORMATION: Description of Artificial Sequence:/note =
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25     actgggggaa aaatcacttt ccagtctgtt ttgcaagggtg tgcatttcca tcttgattcc      120
26     ctgaaagtcc atctgctgca tcggtcaaga gaaactccac ttgcatgaag attgcacgcc      180
27     tgcagcttgc atctttgttg caaaactagc tacagaagag aagcaaggca aagtcttttg      240
28     tgctccccctc ccccatcaaa ggaaagggga aaatgtctca gtcgaaaggc aagaagcgaa      300
29     accctggcct taaaattcca aaagaagcat ttgaacaacc tcagaccagt tccacaccac      360
30     ctagagattt agactccaag gcttgcatth ctattggaaa tcagaacttt gaggtgaagg      420
31     cagatgacct ggagcctata atggaactgg gacgaggtgc gtacggggtg gtggagaaga      480
32     tgcggcacgt gccagcggg cagatcatgg cagtgaagcg gatccgagcc acagtaaata      540
33     gccaggaaca gaaacggcta ctgatggatt tggatatttc catgaggacg gtggactgtc      600
34     cattcactgt caccttttat ggcgcactgt ttcggggagg tgatgtgtgg atctgcatgg      660
35     agctcatgga tacatcacta gataaattct acaaacaagt tattgataaa ggccagacaa      720
36     ttccagagga catcttaggg aaaatagcag tttctattgt aaaagcatta gaacatttac      780
37     atagtaagct gtctgtcatt cacagagacg tcaagccttc taatgtactc atcaatgtct      840
38     tcggtcaagt gaagatgtgc gattttggaa tcagtggcta cttggtggac tctgttgcta      900
39     aaacaattga tgcaggttgc aaaccataca tggcccttga aagaataaac ccagagctca      960
40     accagaaggg atacagtgtg aagtctgaca tttggagtct gggcatcacg atgattgagt      1020
41     tggccatcct tcgatttccc tatgattcat ggggaactcc atttcagcag ctcaaacagg      1080
42     tggtagagga gccatcgcca caactcccag cagacaagtt ctctgcagag tttgttgact      1140
43     ttacctcaca gtgcttaaag aagaattcca aagaacggcc tacataccca gagctaattgc      1200
44     aacatccatt tttcacccta catgaatcca aaggaacaga tgtggcatct tttgtaaaac      1260

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45      tgattcttgg agactaaaaa gcagtggact taatcggttg accctactgt ggattggtgg      1320
46      gtttcggggg gaagcaagtt cactacagca tcaatagaaa gtcactcttg agataattta      1380
47      accctgcctc tcagagggtt ttctctccca attttctttt tactccccct cttaaggggg      1440
48      ccttggaatc tatagtatag aatgaactgt ctagatggat gaattatgat aaaggcttag      1500
49      gacttcaaaa ggtgattaaa tatttaatga tgtgtcatat gaaaaaaaaa aaaaaaaaaa      1560
50      aaaaaaaaaa aaaaaaaaaa aaaaaaa      1587
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53 <211> LENGTH: 334
54 <212> TYPE: PRT
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56 <220> FEATURE:
57 <223> OTHER INFORMATION: Description of Artificial Sequence:/note =
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59 <400> SEQUENCE: 2
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61         1             5             10             15
62     Lys Glu Ala Phe Glu Gln Pro Gln Thr Ser Ser Thr Pro Pro Arg Asp
63         20             25             30
64     Leu Asp Ser Lys Ala Cys Ile Ser Ile Gly Asn Gln Asn Phe Glu Val
65         35             40             45
66     Lys Ala Asp Asp Leu Glu Pro Ile Met Glu Leu Gly Arg Gly Ala Tyr
67         50             55             60
68     Gly Val Val Glu Lys Met Arg His Val Pro Ser Gly Gln Ile Met Ala
69         65             70             75             80
70     Val Lys Arg Ile Arg Ala Thr Val Asn Ser Gln Glu Gln Lys Arg Leu
71         85             90             95
72     Leu Met Asp Leu Asp Ile Ser Met Arg Thr Val Asp Cys Pro Phe Thr
73         100            105            110
74     Val Thr Phe Tyr Gly Ala Leu Phe Arg Glu Gly Asp Val Trp Ile Cys
75         115            120            125
76     Met Glu Leu Met Asp Thr Ser Leu Asp Lys Phe Tyr Lys Gln Val Ile
77         130            135            140
78     Asp Lys Gly Gln Thr Ile Pro Glu Asp Ile Leu Gly Lys Ile Ala Val
79         145            150            155            160
80     Ser Ile Val Lys Ala Leu Glu His Leu His Ser Lys Leu Ser Val Ile
81         165            170            175
82     His Arg Asp Val Lys Pro Ser Asn Val Leu Ile Asn Ala Leu Gly Gln
83         180            185            190
84     Val Lys Met Cys Asp Phe Gly Ile Ser Gly Tyr Leu Val Asp Ser Val
85         195            200            205
86     Ala Lys Thr Ile Asp Ala Gly Cys Lys Pro Tyr Met Ala Pro Glu Arg
87         210            215            220
88     Ile Asn Pro Glu Leu Asn Gln Lys Gly Tyr Ser Val Lys Ser Asp Ile
89         225            230            235            240
90     Trp Ser Leu Gly Ile Thr Met Ile Glu Leu Ala Ile Leu Arg Phe Pro
91         245            250            255
92     Tyr Asp Ser Trp Gly Thr Pro Phe Gln Gln Leu Lys Gln Val Val Glu
93         260            265            270
94     Glu Pro Ser Pro Gln Leu Pro Ala Asp Lys Phe Ser Ala Glu Phe Val

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95          275          280          285
96      Asp Phe Thr Ser Gln Cys Leu Lys Lys Asn Ser Lys Glu Arg Pro Thr
97          290          295          300
98      Tyr Pro Glu Leu Met Gln His Pro Phe Phe Thr Leu His Glu Ser Lys
99      305          310          315          320
100      Gly Thr Asp Val Ala Ser Phe Val Lys Leu Ile Leu Gly Asp
101          325          330
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105 <212> TYPE: DNA
106 <213> ORGANISM: Artificial Sequence
107 <220> FEATURE:
108 <223> OTHER INFORMATION: Description of Artificial Sequence:/note =
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110 <400> SEQUENCE: 3
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112      agccagccca ttgacatccc agatgccaaag aagagaggcc ggaaaaagaa gcgctgtcgg      120
113      gctactgaca gcttctcagg cagggttcgaa gatgtctatc agctgcagga ggatgtgctg      180
114      ggggaagggtg ctcacgctcg tgtgcagacc tgtgtcaatc tcatcaccaa ccaggaatat      240
115      gctgtcaaga tcattgagaa gcagctgggc cacatccgca gcagggtgtt ccgggagggtg      300
116      gagatgctgt accagtgccg gggacatagg aatgttctag aactgattga gttctttgag      360
117      gaggaggacc gtttctacct ggtgtttgag aagatgcgtg gcgcatccat cctaagccac      420
118      atccatagaa ggcgccactt taacgagctg gaggccagcg tggtagtaca ggacgtggcc      480
119      agtgccctgg acttcctgca taacaaaggc atcgccaca gggacctaaa gccagagaac      540
120      atcctatgtg agcaccceaa ccagggtctcg ccagtgaaga tctgcgactt cgaccttggc      600
121      agtggatatca aactcaatgg agactgctcc cccatctcca caccagagct gctcaccccg      660
122      tgtgggtcag ctgagtacat ggccccagag gtgggtggagg ccttcagtga agaggccagc      720
123      atctacgaca agcgtgcga cctgtggagc ctgggcgtca tcctctacat cctgcttagt      780
124      ggctacccgc cttcgtggg ccaactgtggc agcgaactgt gctgggaccg tggggaggcc      840
125      tgtcctgctt gccagaacat gctgtttgag agcatccagg agggcaagta tgagttccct      900
126      gacaaggact ggtcccatc ctcccttgcg gccaaagacc tcatctccaa gctgctggct      960
127      cgagatgcca agcagaggct gagtgtgccc caagtccctg agcatccctg ggtgcagggg      1020
128      tgtgccccag agaacaccct accgacaccc ttggttctgc agaggaacag ctgtgccaaa      1080
129      gacctacgt cctttgcggc tgaggccatc gccatgaacc ggcagctggc ccagtgtgag      1140
130      gaggacgctg ggcaggacca gcctgtggct atccgagcta cctcacgctg cctgcagctg      1200
131      tccccaccct ccaggtccaa gctggccccag cggcgccaga gggctagcct gtcggccacc      1260
132      cctgtgggtc ttgtggggga tcgcgcatga cccccactag ctcttgttac atatgccctt      1320
133      gccccgcggg gcctgaaggc tagggacctg gacacccac cccttgccat tccaggtgcc      1380
134      agctcagctg ggtcctctgg ggggtgtagg gtctgttagg ggggtgtctc ttttctccct      1440
135      gtccctcccc tgccctgccc acttggtttt gttttgtttg ttttctttg ccgctattga      1500
136      aagcaagtgc cgggaggagg gcggagggtc caggccgccc agcctgcacc ccacgatgct      1560
137      cacctgccaa ctgtgaaggc cctgccacct gcgccccac ctccactcca gccactctgc      1620
138      tgtcttccag ggttggggat cccgcagggt cagcacccca cacctctccc agccctcagt      1680
139      gttgtcaggg acaggccctc ctggtgagca cagtgggtgt tgcattctct caccagagca      1740
140      cccttgggtc tggggtaggg cagggtctcc tgtcttggat agagacctct ggggagcagg      1800
141      tggatgggga cagtgcactt gattgacccc gactcccat catccacctg cagtgtccct      1860
142      tggagggttg acaatcagaa acccctccca ggctgcttag ctcttgccc tgggacagac      1920
143      ctactgtctc caacccact tcccaggggc agagctggaa ggggacctg caccagcta      1980
144      gctccaccac agcaggagag gtgctggacc aggttttcat cagcaaakat ggggctccca      2040

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145      catgtctccc caccagggc acctgagtgc cccttctcag ggctcagcct gaccacggcc      2100
146      acgtcctgcc cctgggggttc ctaagctctc ctagctgctt ctgttagcca gagctgaggc      2160
147      catacccagg gctctcacct tcctgttgcc cccagagggc agcagctcag gcgtgcctgc      2220
148      tttcaggaaa gggaggctgg gaagggatgt ggtggccctg cggtgcccag acctaactgc      2280
149      ccgaggcctg tagactgttc tagccgaact actatgcaat acaagttccc attttctcca      2340
150      tggccctgct ggtcgggggc ggctgccagg ggccaggcca cctgcccctg caactgctca      2400
151      ggtgtctaca gggcagcccc tggcctcaaa aatccttggt caggattggt tgtcagattt      2460
152      agtttaggct tttttttttt ttttaaagaa ataatttgac ttgcttccct gttcttgaag      2520
153      agtacttgaa tgtcggggtc tggggtgggg gggcctggga caccactgc ccagcatcct      2580
154      ccaccctcct ccctagctctc ataggatcgt cacagtggag gtgacatgcc ttctccagtc      2640
155      ctgccccacc tgctctgttg gacacatttc caaagaaccc ctgggggttg gacctcctcc      2700
156      atcagtatga ctcagctggt ggccacctga ggactcggcc cccctgcagg ttctgaagc      2760
157      aacctgactg ggcagtgagc agcattgacc cccactcacc cccaaaacag ggctgtgatt      2820
158      tccttagtcc ttccaagccc gacctggagg atgggtcaga ccccttaact gtgaatgaga      2880
159      catgatcctg ggctggcttc gccacaaacc atgcagaaat ctaaaaggcc tgtttagagag      2940
160      tgggggacat gcaagcactt ttaactccat cgtaccaggt gaactgacct ccggactcct      3000
161      ttcccaccaa ctgtcaacgc caggattttg tattctgttt tgtaaggatt taataaaagt      3060
162      catttaaaaa aaaaaaaaaa                                3080

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165 <211> LENGTH: 412

166 <212> TYPE: PRT

167 <213> ORGANISM: Artificial Sequence

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169 <223> OTHER INFORMATION: Description of Artificial Sequence:/note =
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171 <400> SEQUENCE: 4

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175      20          25          30
176      Glu Asp Val Tyr Gln Leu Gln Glu Asp Val Leu Gly Glu Gly Ala His
177      35          40          45
178      Ala Arg Val Gln Thr Cys Val Asn Leu Ile Thr Asn Gln Glu Tyr Ala
179      50          55          60
180      Val Lys Ile Ile Glu Lys Gln Leu Gly His Ile Arg Ser Arg Val Phe
181      65          70          75          80
182      Arg Glu Val Glu Met Leu Tyr Gln Cys Gln Gly His Arg Asn Val Leu
183      85          90          95
184      Glu Leu Ile Glu Phe Phe Glu Glu Glu Asp Arg Phe Tyr Leu Val Phe
185      100         105         110
186      Glu Lys Met Arg Gly Gly Ser Ile Leu Ser His Ile His Arg Arg Arg
187      115         120         125
188      His Phe Asn Glu Leu Glu Ala Ser Val Val Val Gln Asp Val Ala Ser
189      130         135         140
190      Ala Leu Asp Phe Leu His Asn Lys Gly Ile Ala His Arg Asp Leu Lys
191      145         150         155         160
192      Pro Glu Asn Ile Leu Cys Glu His Pro Asn Gln Val Ser Pro Val Lys
193      165         170         175
194      Ile Cys Asp Phe Asp Leu Gly Ser Gly Ile Lys Leu Asn Gly Asp Cys

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195				180				185				190				
196	Ser	Pro	Ile	Ser	Thr	Pro	Glu	Leu	Leu	Thr	Pro	Cys	Gly	Ser	Ala	Glu
197			195					200				205				
198	Tyr	Met	Ala	Pro	Glu	Val	Val	Glu	Ala	Phe	Ser	Glu	Glu	Ala	Ser	Ile
199		210					215					220				
200	Tyr	Asp	Lys	Arg	Cys	Asp	Leu	Trp	Ser	Leu	Gly	Val	Ile	Leu	Tyr	Ile
201		225				230					235					240
202	Leu	Leu	Ser	Gly	Tyr	Pro	Pro	Phe	Val	Gly	His	Cys	Gly	Ser	Asp	Cys
203				245					250						255	
204	Gly	Trp	Asp	Arg	Gly	Glu	Ala	Cys	Pro	Ala	Cys	Gln	Asn	Met	Leu	Phe
205			260					265						270		
206	Glu	Ser	Ile	Gln	Glu	Gly	Lys	Tyr	Glu	Phe	Pro	Asp	Lys	Asp	Trp	Ser
207		275						280				285				
208	His	Ile	Ser	Phe	Ala	Ala	Lys	Asp	Leu	Ile	Ser	Lys	Leu	Leu	Val	Arg
209		290					295					300				
210	Asp	Ala	Lys	Gln	Arg	Leu	Ser	Ala	Ala	Gln	Val	Leu	Gln	His	Pro	Trp
211		305				310					315					320
212	Val	Gln	Gly	Cys	Ala	Pro	Glu	Asn	Thr	Leu	Pro	Thr	Pro	Leu	Val	Leu
213				325					330						335	
214	Gln	Arg	Asn	Ser	Cys	Ala	Lys	Asp	Leu	Thr	Ser	Phe	Ala	Ala	Glu	Ala
215			340					345						350		
216	Ile	Ala	Met	Asn	Arg	Gln	Leu	Ala	Gln	Cys	Glu	Glu	Asp	Ala	Gly	Gln
217		355					360					365				
218	Asp	Gln	Pro	Val	Val	Ile	Arg	Ala	Thr	Ser	Arg	Cys	Leu	Gln	Leu	Ser
219		370				375					380					
220	Pro	Pro	Ser	Gln	Ser	Lys	Leu	Ala	Gln	Arg	Arg	Gln	Arg	Ala	Ser	Leu
221		385			390					395						400
222	Ser	Ala	Thr	Pro	Val	Val	Leu	Val	Gly	Asp	Arg	Ala				
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235	cttcttgctc	agtgccttga	agtttctctg	caatgaactg	acaaatcgga	accatggtgc										180
236	aaaagaagtt	ctgcccctcg	ttacttgact	atctcgtgat	cgtaggggcg	aggcacccaa										240
237	gcagtgcacg	tgtggctcag	actcctgagc	tgctgcggag	gtaccacta	gaggatcacc										300
238	cagagttccc	cctgccccca	gatgtggtgt	tcttctgcc	gccagaagga	tgtctgagt										360
239	tgcggcagcg	gcggatgagc	cttcgggacg	atacctcttt	tgtcttcacc	ctaaccgata										420
240	aggacaccgg	agtcaccgcg	tatggcatct	gtgtcaactt	ctaccgttcc	ttccaaaagc										480
241	gaatgccaaa	ggaaaagggtg	gaaggcggag	caggaccccg	tgggaaggaa	ggcgctcaca										540
242	cctctggtgc	ctcagaagag	gctgccgctg	ggagctcaga	gagtggctca	accttgacgc										600
243	cgcctagtgc	tgactccact	cctgacgtaa	accagtctcc	tcggggcaaa	cgtagggcaa										660
244	aagcgggcag	ccgctcccgc	aacagtaccc	tgacatccct	gtgtgtgctt	agccactacc										720

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